

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/192,102

1816

DATE: 07/18/97
TIME: 15:50:38

INPUT SET: S19077.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Le, Junming
Vilcek, Jan
Daddona, Peter E.
Ghrayeb, John
Knight, David M.
Siegel, Scott A.

(ii) TITLE OF INVENTION: ANTI-TNF ANTIBODIES AND ASSAYS EMPLOYING
ANTI-TNF ANTIBODIES

(iii) NUMBER OF SEQUENCES: 19

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
(B) STREET: Two Militia Drive
(C) CITY: Lexington
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 02173

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/192,102
(B) FILING DATE: 04-FEB-1994
(C) CLASSIFICATION: 424

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US/08/192,093
(B) FILING DATE: 04-FEB-1994

(A) APPLICATION NUMBER: US 08/013,413
(B) FILING DATE: 02-FEB-1993

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/010,406
(B) FILING DATE: 29-JAN-1993

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PATENT APPLICATION US/08/192,102DATE: 07/18/97
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47 (vii) PRIOR APPLICATION DATA:
48 (A) APPLICATION NUMBER: US 07/943,852
49 (B) FILING DATE: 11-SEP-1992
50
51 (vii) PRIOR APPLICATION DATA:
52 (A) APPLICATION NUMBER: US 07/853,606
53 (B) FILING DATE: 18-MAR-1992
54
55 (vii) PRIOR APPLICATION DATA:
56 (A) APPLICATION NUMBER: US 07/670,827
57 (B) FILING DATE: 18-MAR-1991
58
59 (viii) ATTORNEY/AGENT INFORMATION:
60 (A) NAME: Brook, David E.
61 (B) REGISTRATION NUMBER: 22,592
62 (C) REFERENCE/DOCKET NUMBER: NYU93-01M3
63
64 (ix) TELECOMMUNICATION INFORMATION:
65 (A) TELEPHONE: (617) 861-6240
66 (B) TELEFAX: (617) 861-9540
67
68
69 (2) INFORMATION FOR SEQ ID NO:1:
70
71 (i) SEQUENCE CHARACTERISTICS:
72 (A) LENGTH: 157 amino acids
73 (B) TYPE: amino acid
74 (D) TOPOLOGY: linear
75
76 (ii) MOLECULE TYPE: peptide
77
78 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
79
80 Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val
81 1 5 10 15
82
83 Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
84 20 25 30
85
86 Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
87 35 40 45
88
89 Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
90 50 55 60
91
92 Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
93 65 70 75 80
94
95 Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
96 85 90 95
97
98 Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
99 100 105 110

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100
101 Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys
102      115                      120                      125
103
104 Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
105      130                      135                      140
106
107 Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
108      145                      150                      155
109
110

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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131
132 GAC ATC TTG CTG ACT CAG TCT CCA GCC ATC CTG TCT GTG AGT CCA GGA      48
133 Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
134   1                      5                      10                      15
135
136 GAA AGA GTC AGT TTC TCC TGC AGG GCC AGT CAG TTC GTT GGC TCA AGC      96
137 Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
138      20                      25                      30
139
140 ATC CAC TGG TAT CAG CAA AGA ACA AAT GGT TCT CCA AGG CTT CTC ATA     144
141 Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
142      35                      40                      45
143
144 AAG TAT GCT TCT GAG TCT ATG TCT GGG ATC CCT TCC AGG TTT AGT GGC     192
145 Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
146      50                      55                      60
147
148 AGT GGA TCA GGG ACA GAT TTT ACT CTT AGC ATC AAC ACT GTG GAG TCT     240
149 Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
150      65                      70                      75                      80
151
152 GAA GAT ATT GCA GAT TAT TAC TGT CAA CAA AGT CAT AGC TGG CCA TTC     288

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153 Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
154 85 90 95
155
156 ACG TTC GGC TCG GGG ACA AAT TTG GAA GTA AAA 321
157 Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys
158 100 105
159

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

171 Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
172 1 5 10 15
173
174 Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
175 20 25 30
176
177 Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
178 35 40 45
179
180 Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
181 50 55 60
182
183 Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
184 65 70 75 80
185
186 Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
187 85 90 95
188
189 Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys
190 100 105
191

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..357

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206
207
208      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
209
210      GAA GTG AAG CTT GAG GAG TCT GGA GGA GGC TTG GTG CAA CCT GGA GGA      48
211      Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
212      1          5          10          15
213
214      TCC ATG AAA CTC TCC TGT GTT GCC TCT GGA TTC ATT TTC AGT AAC CAC96
215      Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His
216      20          25          30
217
218      TGG ATG AAC TGG GTC CGC CAG TCT CCA GAG AAG GGG CTT GAG TGG GTT      144
219      Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val
220      35          40          45
221
222      GCT GAA ATT AGA TCA AAA TCT ATT AAT TCT GCA ACA CAT TAT GCG GAG 192
223      Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
224      50          55          60
225
226      TCT GTG AAA GGG AGG TTC ACC ATC TCA AGA GAT GAT TCC AAA AGT GCT      240
227      Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala
228      65          70          75          80
229
230      GTC TAC CTG CAA ATG ACC GAC TTA AGA ACT GAA GAC ACT GGC GTT TAT      288
231      Val Tyr Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr
232      85          90          95
233
234      TAC TGT TCC AGG AAT TAC TAC GGT AGT ACC TAC GAC TAC TGG GGC CAA      336
235      Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln
236      100          105          110
237
238      GGC ACC ACT CTC ACA GTC TCC      357
239      Gly Thr Thr Leu Thr Val Ser
240      115
241
242

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(2) INFORMATION FOR SEQ ID NO:5:

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243
244
245      (i) SEQUENCE CHARACTERISTICS:
246          (A) LENGTH: 119 amino acids
247          (B) TYPE: amino acid
248          (D) TOPOLOGY: linear
249
250      (ii) MOLECULE TYPE: protein
251
252      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
253
254      Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
255      1          5          10          15
256
257      Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His
258      20          25          30

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/192,102

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Original Text